



SEQUENCE LISTING

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*Sub
D*
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Raleigh, Elisabeth A.

<120> Method For Cloning And Producing The MseI Restriction Endonuclease

<130> NEB-181

D <140> US 09/689,343
<141> 2000-10-12

<160> 9

<170> PatentIn version 3.1

<210> 1
<211> 903
<212> DNA
<213> Micrococcus sp.

<220>
<221> CDS
<222> (1)..(900)
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gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc 96
Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
20 25 30

cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg 144
Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
35 40 45

ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc 192
Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
50 55 60

ttc aaa ggc cag acg tac gac acg gtc aag acg act ctg cac tcg tat 240
Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
65 70 75 80

gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg 288
Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
85 90 95

gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu 100 105 110	336
gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe 115 120 125	384
gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly 130 135 140	432
gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val 145 150 155 160	480
tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp 165 170 175	528
cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala 180 185 190	576
ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro 195 200 205	624
gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile 210 215 220	672
atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu 225 230 235 240	720
gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg cgc cag ctc Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu 245 250 255	768
gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val 260 265 270	816
atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile 275 280 285	864
gtg cag act ccc cag agt gac cca cga acc gac gga tga Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly 290 295 300	903

<210> 2
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<212> PRT
<213> *Micrococcus* sp.

<400> 2

Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
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Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
20 25 30

Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
35 40 45

Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
50 55 60

Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
65 70 75 80

Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
85 90 95

Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
100 105 110

Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
115 120 125

Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
130 135 140

Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
145 150 155 160

Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
165 170 175

Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
180 185 190

Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
195 200 205

Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
210 215 220

Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
225 230 235 240

Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
245 250 255

Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
260 265 270

Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
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Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
 290 295 300

<210> 3
 <211> 1236
 <212> DNA
 <213> Unknown

<220>
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 <221> misc_feature
 <222> (198)..(198)
 <223> Xaa = any amino acid

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 <222> (594)..(594)
 <223> N= G, A, C or T

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1 5 10 15	
acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg	96
Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro	
20 25 30	
cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg	144
Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu	
35 40 45	
ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct	192
Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro	
50 55 60	
ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat	240
Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp	
65 70 75 80	
tcg cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag	288
Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu	
85 90 95	
tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta	336
Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val	
100 105 110	

ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu 115 120 125	384
gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe 130 135 140	432
ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro 145 150 155 160	480
tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val 165 170 175	528
tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln 180 185 190	576
cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala 195 200 205	624
ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp 210 215 220	672
tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly 225 230 235 240	720
tat ccg actcaa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Ala 245 250 255	768
tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly 260 265 270	816
aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn 275 280 285	864
gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg 290 295 300	912
gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro 305 310 315 320	960
atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile 325 330 335	1008

cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gta gac gat caa	1056
Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln	
340 345 350	
tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc	1104
Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg	
355 360 365	
ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg	1152
Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu	
370 375 380	
ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca	1200
Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr	
385 390 395 400	
ggt cga gcc gat agc cct cac ccc gta tcg ttt tga	1236
Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe	
405 410	

<210> 4
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<213> Unknown

<220>
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<220>
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<222> (198)..(198)
<223> Xaa = any amino acid

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Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
20 25 30

Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
35 40 45

Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
50 55 60

Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
65 70 75 80

Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
85 90 95

Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
100 105 110

Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
115 120 125

Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
130 135 140

Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
145 150 155 160

Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
165 170 175

Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
180 185 190

Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
195 200 205

Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
210 215 220

Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
225 230 235 240

Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
245 250 255

Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
260 265 270

Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
275 280 285

Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
290 295 300

Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
305 310 315 320

Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
325 330 335

Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
340 345 350

Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
355 360 365

Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
370 375 380

Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
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Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
405 410

<210> 5
<211> 924
<212> DNA
<213> Unknown

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gcc gac aac atg gaa gtc ctg cga ggg ctt ccg gcg gcg tcc gtg gac	96
Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp	
20 25 30	
ctg atc tac atc gat cct ccg ttc aac acc gga aag gtt cag gag cgc	144
Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg	
35 40 45	
act cag ctc aaa acg gtg cgc tcc gag tgg ggc gat cgc gtc gga ttc	192
Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe	
50 55 60	
cag ggc cgt cgc tac gaa agc atc gtc gtg ggt aag aag cgc ttt acc	240
Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr	
65 70 75 80	
gac ttc ttc gac gac tat ctg gct ttc ctg gaa ccg cgc ctg gtc gaa	288
Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu	
85 90 95	
gcc cat cgt gtt ctg gcg ccg cac ggg tgc ctc tac ttt cac gtc gac	336
Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp	
100 105 110	
tac cgc gag gtg cac tac tgt aag gtc ctt ctt gac ggc atc ttc ggt	384
Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly	
115 120 125	
cgc gag gcc ttt ctc aac gag atc atc tgg gcc tac gat tac ggc ggg	432
Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly	
130 135 140	
cgt ccg aag gac agg tgg cct cct aag cac gac aac atc ctg ctc tac	480
Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr	
145 150 155 160	

gcc aag act ccc ggt cgc cac gtg ttc aat gcg gac gaa atc gag cgc	528
Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg	
165 170 175	
att ccc tac atg gct ccg ggc ctg gtt ggc ccc gaa aag gca gcc cgt	576
Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg	
180 185 190	
gga aaa ctg cca acc gac acg tgg tgg cat acg atc gtt ccg acc agc	624
Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser	
195 200 205	
ggc tcc gag aag acc ggg tat cca acc cag aaa cct tta ggg att ctc	672
Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu	
210 215 220	
cgc cgt att gtg cag gca tcg tct cat ccg ggg gca gtc gtg ctc gac	720
Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp	
225 230 235 240	
ttc ttc gcc ggc agt ggg aca aca ggg gta gcg gct ttt gag ttg ggc	768
Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly	
245 250 255	
cg ^g cgt ttc att ctg gtc gat aac cat ccg gag gcc ctc cag gtg atg	816
Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met	
260 265 270	
gcc agg cgc ttc gac ggc atc gag ggg atc gaa tgg gtg ggc ttc gat	864
Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp	
275 280 285	
ccg aca ccg tac cag aag ggc gca aag cag cgc cgc tcc tgc ccg gcg	912
Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala	
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ccc acc ggg taa	924
Pro Thr Gly	
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<210> 6
<211> 307
<212> PRT
<213> Unknown

<220>
<223> Environmental DNA

<400> 6

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20 25 30	

Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg
35 40 45

Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
50 55 60

Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
65 70 75 80

Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
85 90 95

Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
100 105 110

Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
115 120 125

Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
130 135 140

Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
145 150 155 160

Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
165 170 175

Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
180 185 190

Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
195 200 205

Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
210 215 220

Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
225 230 235 240

Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
245 250 255

Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
260 265 270

Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
275 280 285

Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala
290 295 300

Pro Thr Gly
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<210> 7
<211> 561
<212> DNA
<213> *Micrococcus* sp.

<220>
<221> CDS
<222> (1)..(558)
<223>

<400> 7

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Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala	
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agc gcg gcg aac ctc gct gat cggt tac gta gcg agt gaa gac gac ccc	96
Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro	
20 25 30	
tgg gtc ggc agc ccg ttc gag tgg atc ctt cgc gtt cca tcc aga acg	144
Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr	
35 40 45	
aag ggc gcg gtc ggt gag ctg ctc gtg agc gaa tgg gct aat gcc aaa	192
Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys	
50 55 60	
ggc ctc cgt gtg aag agg tcg ggg tcc agc gat gcg gac cgc gtg atc	240
Gly Leu Arg Val Lys Arg Ser Gly Ser Asp Ala Asp Arg Val Ile	
65 70 75 80	
aac ggg cat cgc atc gag atc aag atg tcg act ttg tgg aag tcc ggc	288
Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly	
85 90 95	
ggc ttc aag ttt cag cag atc cgg gat cag gag tac gac ttt tgc ctc	336
Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu	
100 105 110	
tgc ctt ggg atc agc ccg ttc gaa gtg cac gcg tgg ctg ctg ccc aaa	384
Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys	
115 120 125	
gac cta ttg ctt gag tac gtg att ggt cac atg ggt cag cac acc ggc	432
Asp Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly	
130 135 140	
gcg agc ggg agc gac act gcg tgg ctg ggg ttc cca gcg gac gag ccg	480
Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro	
145 150 155 160	
tat gac tgg atg cgc cct ttc gga ggt cgc tta ggt cac gtc gaa gat	528
Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp	
165 170 175	

ctc ctc ctc gcg gcc ggc ccc ggt ccc tac tga
Leu Leu Leu Ala Ala Gly Pro, Gly Pro Tyr
180 185

561

<210> 8
<211> 186
<212> PRT
<213> Micrococcus sp.

<400> 8

Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala
1 5 10 15

Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
20 25 30

Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
35 40 45

Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
50 55 60

Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
65 70 75 80

Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
85 90 95

Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
100 105 110

Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
115 120 125

Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
130 135 140

Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
145 150 155 160

Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
165 170 175

Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
180 185

<210> 9
<211> 413
<212> DNA
<213> Escherichia coli

<400> 9

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60

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ccggtttttt ttgcgttcaa tttgtcattt tgtccgtgg tgtttaaacc gcacagaata	180
aattgtcgta atttcacctt taaaataaaa taaaaagaga aaaaaattct ctgtgaaagg	240
gctatgttag ataaaattga ccgtaagctg ctggcattac tgcaacgagg ttgcaccctc	300
tcttgagg cactggctga agccgttaat ctgacaacca ccccttgctg gaagcgctg	360
aaacggctgg aggacgacgg tattttatc ggcaaagtgc ccctgctgga tcc	413

D
done